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ICA-BASED SEGMENTATION OF THE BRAIN ON PERFUSION DATA

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Abstract-**An Independent Component Analysis (ICA) based segmentation technique is presented allowing the quantitative assessment of cerebral blood volume (CBV), cerebral blood flow (CBF) and mean transit time (MTT) from dynamic susceptibility contrast magnetic resonance (MR) images of the brain. Tissue types such as gray matter (GM), white matter (WM), and pathology appear as different ICA components as a result of their distinct temporal response to the first passage of contrast agent through the brain. The average CBV, CBF, and MTT values calculated for each component / tissue type could help evaluate the evolution of pathology and provide the opportunity for intersubject comparisons.**

***Keywords* – Independent Component Analysis, Segmentation, Magnetic Resonance Imaging Perfusion, Dynamic Susceptibility Contrast Imaging,**

I. INTRODUCTION

The segmentation of perfusion images is essential for tissue-specific quantitative assessment of cerebral blood volume (CBV), cerebral blood flow (CBF), and mean transit time (MTT) values. Average CBV, CBF, MTT values expressed per tissue type can help assess the severity of pathology and the progression of disease. Other researchers have applied a similarity-based segmentation method to perfusion data using a reference model curve [1]. The determination of the reference curve however requires that the user identify the voxels of interest making the method somewhat subjective. Independent Component Analysis (ICA) [2] is a model-free method that can group together temporal responses based on their distinct spatial signatures without requiring a reference model. ICA, for example, has been used in functional magnetic resonance imaging (fMRI) analysis for the determination of activation patterns [3, 4]. ICA has also been applied to perfusion data for the identification of large arteries in order to eliminate their confounding effects [5]. In this work, ICA is applied to dynamic susceptibility contrast-based perfusion data to segment the brain, based on temporally distinct patterns of perfusion responses.

II. METHODOLOGY

Perfusion

Time-series data were acquired during pre and post-injection of an intravenous dose of the contrast agent Gd-DTPA. The images were obtained on a 1.5 Tesla MRI system retrofitted for echo-planar imaging (TR = 2 sec, TE = 60 msec). The ICA analysis was applied to both susceptibility and concentration time curves. The signal intensity time course of dynamic susceptibility curves is characterized by an initial post-injection loss of signal intensity during the passage of contrast agent and a subsequent recovery (Fig. 1). For the calculation of perfusion parameters, the Perfusion module of the MEDx Analysis Package (Sensor Systems, Sterling VA) was used. Initially the susceptibility curves

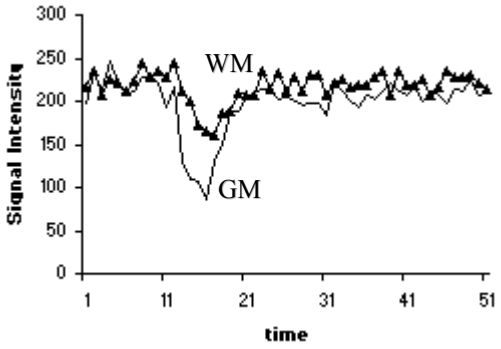

Fig. 1. Representative dynamic susceptibility temporal plots from WM and GM tissue types

were converted into concentration curves via [6],

$$C(t) = -k/TE*\ln[S(t)/S_0] \quad (1)$$

where C(t) is the Gd-DTPA concentration as a function of time; k is a proportionality constant; TE is the echo time; and S(t) and S_0 refer to the recorded signal over time and the average baseline signal intensity prior to the injection of contrast. The images were masked to eliminate non-brain voxels. The concentration-time curves at each voxel were subsequently fitted to gamma variate curves [7]. The fitted gamma variates were evaluated for early arrival time, large area, narrow peak width (low variance in time), and steep slope uptake (high positive skew) for an automated determination of a representative arterial input function (AIF) [9]. The representative AIF was then deconvolved from the observed concentration curves $C_{obs}(t)$ at each voxel using SVD to determine the residue function R(t). The maximum amplitude of the residue function constituted the CBF [10].

$$C_{obs}(t) = CBF\ (R(t)\ *\ AIF(t)) \quad (2)$$

For the determination of absolute CBV, a Wiener filter-like approach was adopted whereby the area under the concentration curve was normalized both by the area under the AIF and by the density of the brain tissue ρ, and multiplied by a correction factor K_h that took into account the difference in hematocrit between large and small vessels [11]. The ratio of CBV to CBF constituted the MTT.

$$CBV_{abs} = \frac{Kh}{\rho}\frac{\int C(t)dt}{\int AIF(t)dt} \quad (3)$$

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Abstract

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Independent Component Analysis

The ICA analysis was conducted assuming that the perfusion profiles within each tissue type were similar but that the profiles varied between tissue types. Thus it was assumed that the individual voxel time courses could be represented as a linear mixture of the susceptibility responses or the concentration time curves and other spatially localized and temporally consistent effects. Each voxel time course was expressed using a latent variables model as

$$x_i(t) = \sum_k a_k(t) s_{ki} + \varepsilon_i(t), \qquad (4)$$

where x_i, the perfusion curve associated with voxel *i*, is being expressed as a linear combination of k unknown individual time courses $a_k(t)$ (weighted by the unknown coefficients s_{ki}) plus voxel-specific spatially uncorrelated Gaussian noise $\varepsilon_i(t)$. The coefficients s_{ki} form a set of spatial maps s_k which are assumed to be statistically independent with non-Gaussian distribution. The individual voxel time courses (i.e. susceptibility or concentration curves) were de-meaned and optionally scaled to unit variance. The perfusion data set was then rearranged to form a data matrix X containing the time courses of the individual voxels as columns. When all voxels are considered simultaneously, equation (4) becomes

$$X = A S + \varepsilon. \qquad (5)$$

Since ε is assumed to be jointly Gaussian, to account for the possible existence of non-Gaussian artifactual sources in the data, the number of spatial components was allowed to be larger than the number of different tissue types of interest. The determination of the rank *r* of A then became a problem of model order selection which was solved employing Bayesian model selection by viewing the latent variables model of (4) as a probabilistic principal component analysis (PCA) model [13]. This involved calculating the eigenvalue-decomposition of the sample covariance matrix C_X of the observations

$$C_X = AA^T + C_x \qquad (6)$$

in order to obtain the posterior probability of the data for each possible dimensionality to form maximum a posteriori (MAP) estimates of the 'true' rank *r*, i.e. the dimensionality of the principal signal sub-space of the data assuming Gaussian noise The data was then centered, whitened, and projected into the subspace spanned by the *r* largest eigenvectors of the covariance matrix C_X. The new matrix was decomposed into the product of a mixing matrix A and the matrix of underlying source components S using a fixed-point technique that maximizes approximations to negentropy as a measure of non-Gaussianity [12]. This method was implemented as part of FSL (FMRIB's Software Library, www.fmrib.ox.ac.uk/fsl) [4] which is also incorporated into the MEDx software (Sensor Systems, Sterling VA).

III. Results

The ICA analysis successfully identified GM, WM, CSF, and pathology as different ICA components. The GM/WM - segmentation of the brain depicted in Fig. 2b was obtained

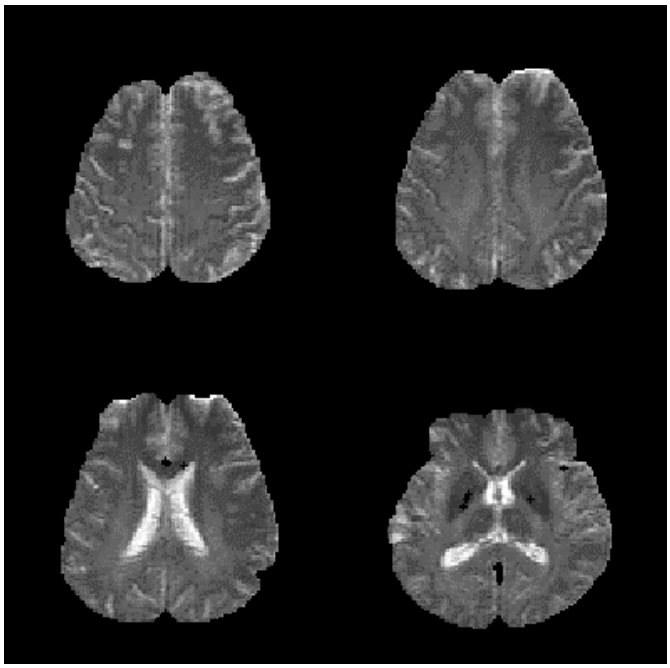

Fig. 2a

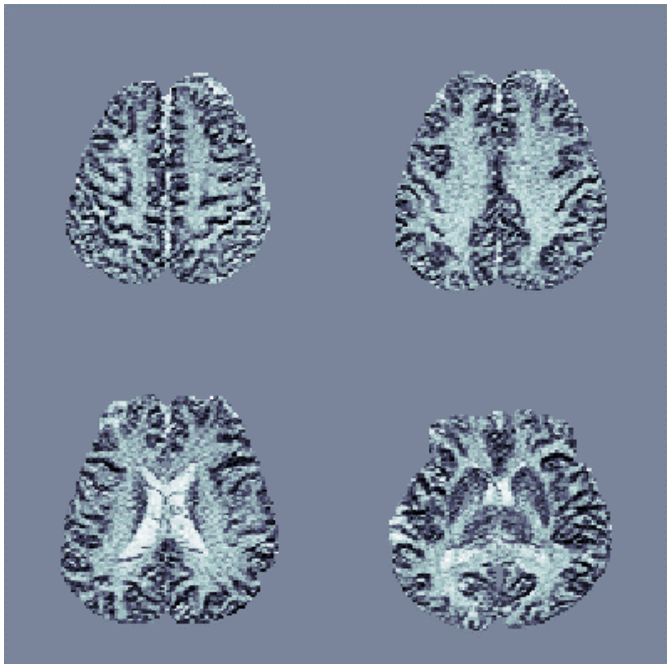

Fig 2b

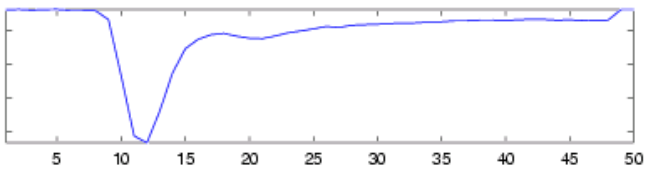

Fig 2c

Fig. 2 (a) The original susceptibility data (b) the ICA component depicting the GM/WM contrast and (c) the corresponding time course.

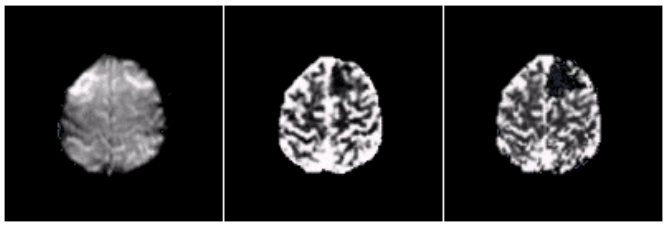

Fig. 3a Fig. 3b Fig. 3c

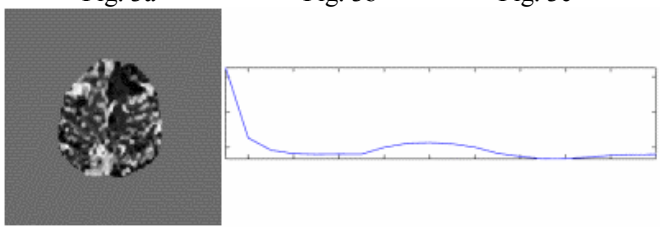

Fig. 3d

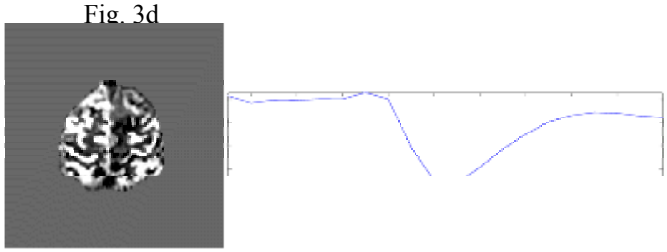

Fig. 3e

Fig. 3 (a) The original stroke data and the associated (b) CBV and (c) CBF maps obtained as a result of the perfusion analysis. (d) the ICA component depicting the lesion and the corresponding time course (e) the ICA component depicting the GM/WM and the corresponding time course

through a three component ICA analysis of variance normalized concentration data. Note that while there is some gray/white matter contrast in parts of the original images (Fig. 2a), the contrast is not consistent spatially, and is clearly inferior to the contrast shown in the relevant spatial ICA map. The temporal curve associated with this component (Fig. 2c) resembles closely that of a susceptibility curve, but is relatively noise-free enabling a clean segmentation. Fig. 3 depicts the case of a stroke patient. Note that in the MR acquisition images, the region of the stroke is not readily visible (Fig. 3a). The lesion is much better delineated in the CBV and CBF maps (Figs. 3b and 3c, respectively) due to the much lower CBV, CBF values in the region of the stroke. The time course associated with the ICA component depicting the lesion (Fig. 3d) has a much flatter response than the time course associated with the component delineating the GM/WM. The quality of the GM/WM segmentation was higher when the ICA analysis was conducted on concentration data as opposed to susceptibility data. In all cases variance normalization increased the contrast and hence the quality of the segmentation maps. The CSF, on the other hand, cannot be delineated using ICA due to the fact that there is no consistent temporal response within that class. It can however, be visualized in one of the ICA components when the analysis is performed on data where the mean intensity image of the raw data is retained. The component map after ICA analysis then reflects the mean image intensities and using it for CSF segmentation is comparable to using the raw image intensities. Applying the binarized ICA segmentation results to the perfusion maps, GM to WM ratios of ~2:1 were obtained both for average CBV and CBF values in the elderly subjects studied as well as in the stroke study.

IV. Discussion

In the segmentation of perfusion maps, it might be argued that the CBV, CBF maps themselves provide an intrinsic segmentation and that thresholding these maps should obviate the need for additional segmentation. Histograms of the CBV and CBF distributions however revealed that the histograms were comprised of a continuum of values and the distributions were unimodal making the determination of a proper threshold totally arbitrary. The ability of ICA to accentuate different tissue types in different components significantly enhanced the quality of the segmentation.

The ICA segmentation results were altered depending on whether the analysis was conducted on susceptibility or on concentration data. Converting the susceptibility data to concentration (Eq. 1) preconditions the data in a way that improves the within-tissue temporal response homogeneity, making it possible for more information to be gleaned by the same number of ICA components, thus improving GM/WM segmentation.

The optimal number of ICA components was determined prior to applying ICA, through Bayesian model selection. Performing the ICA analysis with more than the optimal number of components can split the same information into several components leading to sub-optimal segmentation contrast. It should be noted, however, that in the context of image segmentation such splittings into different component maps may provide useful information as they may reflect valid spatial variations in the temporal responses. In practice, we found our method to be robust, i.e. the splitting of interesting components did not occur until substantially more components were requested than the number suggested by the automatic model-selection procedure.

V. Conclusion

Applying ICA analysis to MR dynamic susceptibility contrast data highlights different tissue types in different ICA components providing good quality segmentation of the brain. The analysis method is fast, robust and the decomposition into different spatial maps and the corresponding time-courses is accomplished without user intervention and no knowledge of the expected temporal response profiles.

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